# RAW SEQUENCE LISTING ERROR REPORT

*RECEIVED*

*JAN 24 2001*

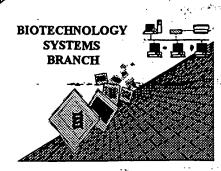*TECH CENTER 1600/29*

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/664,827_

Source: _OIPE_

Date Processed by STIC: _9/26/2000_

## THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

## PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**

2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

## Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
**http://www.uspto.gov/web/offices/pac/checker**

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~~TECH CENTER 1600/2900~~ OIPE

**Does Not Comply**
**Corrected Diskette Needed**

```
            RAW SEQUENCE LISTING              DATE: 09/26/2000
            PATENT APPLICATION:  US/09/664,827   TIME: 12:03:32

            Input Set : A:\SeqList.txt
            Output Set: N:\CRF3\09262000\I664827.raw

   3 <110> APPLICANT: Erikson, Glen
   5 <120> TITLE OF INVENTION: QUADRUPLEX DNA SYSTEM
   7 <130> FILE REFERENCE: E1047/20044
   9 <140> CURRENT APPLICATION NUMBER: US/09/664,827
   9 <141> CURRENT FILING DATE: 2000-09-19
   9 <160> NUMBER OF SEQ ID NOS: 15
  11 <170> SOFTWARE: PatentIn version 3.0
  13 <210> SEQ ID NO: 1
  14 <211> LENGTH: 50
  15 <212> TYPE: DNA
  16 <213> ORGANISM: synthetic construct
  18 <400> SEQUENCE: 1
  19 gagcaccatg acagacactg tcatctctgg tgtgtcctac gatgactctg      50
  22 <210> SEQ ID NO: 2
  23 <211> LENGTH: 50
  24 <212> TYPE: DNA
  25 <213> ORGANISM: synthetic construct
  27 <400> SEQUENCE: 2
  28 cagagtcatc gtaggacaca ccagagatga cagtgtctgt catggtgctc      50
  31 <210> SEQ ID NO: 3
  32 <211> LENGTH: 50
  33 <212> TYPE: DNA
  34 <213> ORGANISM: synthetic construct
  36 <400> SEQUENCE: 3
  37 gagcaccatg acagacactg tcgtctctgg tgtgtcctac gatgactctg      50
  40 <210> SEQ ID NO: 4
  41 <211> LENGTH: 50
  42 <212> TYPE: DNA
  43 <213> ORGANISM: synthetic construct
  45 <400> SEQUENCE: 4
  46 cagagtcatc gtaggacaca ccagagacga cagtgtctgt catggtgctc      50
  49 <210> SEQ ID NO: 5
  50 <211> LENGTH: 50
  51 <212> TYPE: DNA
  52 <213> ORGANISM: synthetic construct
  54 <400> SEQUENCE: 5
  55 gagcaccatg acagacactg tcttctctgg tgtgtcctac gatgactctg      50
  58 <210> SEQ ID NO: 6
  59 <211> LENGTH: 50
  60 <212> TYPE: DNA
  61 <213> ORGANISM: synthetic construct
  63 <400> SEQUENCE: 6
  64 cagagtcatc gtaggacaca ccagagaaga cagtgtctgt catggtgctc      50
  67 <210> SEQ ID NO: 7
  68 <211> LENGTH: 50
  69 <212> TYPE: DNA
  70 <213> ORGANISM: synthetic construct
```

*[Handwritten annotations:]*

OK

per new Sequence Rules, the only valid responses are: Unknown, Artificial Sequence, or scientific name (Genus/species)

(see circled portion of Item 12 on Error Summary sheet)

global error

```
 72 <400> SEQUENCE: 7
 73 gagcaccatg acagacactg tcatctttgg tgtgtcctac gatgactctg        50
 76 <210> SEQ ID NO: 8
 77 <211> LENGTH: 50
 78 <212> TYPE: DNA
 79 <213> ORGANISM: synthetic construct
 81 <400> SEQUENCE: 8
 82 cagagtcatc gtaggacaca ccaaagatga cagtgtctgt catggtgctc        50
 85 <210> SEQ ID NO: 9
 86 <211> LENGTH: 50
 87 <212> TYPE: DNA
 88 <213> ORGANISM: synthetic construct
 90 <400> SEQUENCE: 9
 91 gagcaccatg acagacactg tcatccctgg tgtgtcctac gatgactctg        50
 94 <210> SEQ ID NO: 10
 95 <211> LENGTH: 50
 96 <212> TYPE: DNA
 97 <213> ORGANISM: synthetic construct
 99 <400> SEQUENCE: 10
100 cagagtcatc gtaggacaca ccagggatga cagtgtctgt catggtgctc        50
103 <210> SEQ ID NO: 11
104 <211> LENGTH: 15
105 <212> TYPE: DNA
106 <213> ORGANISM: synthetic construct
108 <400> SEQUENCE: 11
109 ctgtcatctc tggtg                                             15
112 <210> SEQ ID NO: 12
113 <211> LENGTH: 15
114 <212> TYPE: DNA
115 <213> ORGANISM: synthetic construct
117 <400> SEQUENCE: 12
118 caccagagat gacag                                             15
121 <210> SEQ ID NO: 13
122 <211> LENGTH: 15
123 <212> TYPE: DNA
124 <213> ORGANISM: synthetic construct
126 <400> SEQUENCE: 13
127 gacagtagag accac                                             15
130 <210> SEQ ID NO: 14
131 <211> LENGTH: 15
132 <212> TYPE: DNA
133 <213> ORGANISM: synthetic construct
135 <400> SEQUENCE: 14
136 gtggtctcta ctgtc                                             15
139 <210> SEQ ID NO: 15
140 <211> LENGTH: 50
141 <212> TYPE: DNA
142 <213> ORGANISM: synthetic construct
144 <400> SEQUENCE: 15
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RAW SEQUENCE LISTING                    DATE: 09/26/2000
PATENT APPLICATION:   US/09/664,827      TIME: 12:03:32

Input Set : A:\SeqList.txt
Output Set: N:\CRF3\09262000\I664827.raw

145 cagagtcatc gtaggacaca ccagcgatga cagtgtctgt catggtgctc                    50

```
                VERIFICATION SUMMARY              DATE: 09/26/2000
                PATENT APPLICATION:  US/09/664,827   TIME: 12:03:33

                Input Set : A:\SeqList.txt
                Output Set: N:\CRF3\09262000\I664827.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
```

# Raw Sequence Listing Error Summary

ERROR DETECTED    SUGGESTED  CORRECTION        SERIAL NUMBER: _09/664,827_

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
**<210>  sequence id number**
**<400>  sequence id number**
**000**

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings
**Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"**
**Please explain source of genetic material in <220> to <223> section.**
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.